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Figure 5 (cont)

agaataatgtagttcggatccaacgggtgggtggattttcgaaatacacaaatgattcctcctccgat
gaacgggtacgatoagttatcttcttcaatcagatcatcatcagaggagccaagggtttcctttat
gatcatagaatcgctagaggagcttcagtttctgottctagtaactactattaatccttatttca
acgaggcaacaaatcatacgggtactaagtatagtcattttattaatactcattataggtatat
atgtatataactggtgatcttatttgatttaactgggtgggttttagggagccaatggagggaatttg
ggagctacatggaaggaaaccctagaaatggatcaggagggtgtgaaggagtacgaggttttttcc
ggggaaatatggtgaaagagtttcagtggtgggttaaaaogtctgtoactcgttaggtgattgcagt
cotaataccattgattttgtccttgaagctttaaagtttttatctttctatattgatttaaaaca
aatcgtctcttttaagaaaaaacatttttaagtagatgaaagtaagaaacagaaagaaaaaaaga
gagagccttttttgggtgtatgcacctctgagagctgagtcgaagaaagattcagcttttggatta
cccttttgggtgtttattatgagattotaacctaacaactcagacatatatgtttctgttctctt
ccttaattgttgtcatgaaacttctc

FIG. 5 (cont)

ttcccttctctctctcttatotaaaaagaggttccgagagaagaagatcatcatcaatgggogacttct
ctcttctttoatgtcaacagatcaaaaactccgctcggaaccaccaacgatcttcttgagaaacaccc
gtcttgtcgtcaacagctccggcgagatccggacagagacactgaagagtcgtggtcggaacc
aggatcgaagacagggtcagcaaaaacagaagaaaccaacggttgagaggaatgggtgtagcaaa
ctcgagcgtcagagaaatcgaagaagaaaagaagcaactcgcgcgcgcacagtccggagacacgt
catcagtagcatcgatctcttaacaacgotaacccgtttaaccgtacccggtagacccgggtgttgt
gctacaaggcttcccaagctcactcgggagcaacaggatctattgtggtggagtcgggtcgggt
cagggttatgatcgacccgggttatttctccatgggggttttgttgagacctcctccactactcatg
agctctcttcaatctcaaatcctcaaatgtttaaacgttcttccaantaatcgctgtgacacttg
cttcaagggttgtttgttttttaatcgttttcatcaacatgattgatataatataagtttttgc
acttgaaaaagttttgatttttatttatgttaaaaaactgcagaagaacagtttggatggtgac

[illegible]

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FIGURE 5

-2690

cggaatcccaagaatctttctatgcctgcctaaaccoagcaatataaatcaaaccttcacacgct
tcgggtctctcttttacacgtgccggaaaaaaaccctagtagtagccgcccaatgaccatctaaa
gtgggtcccgatgatgacacgtgtcagttggaccactatccgtaacttaacatgaaagcacatgt
gggggtccctcttttcgtccctttgccctaccagttcccttgctctagcccacaatacaatctacggt
gtatctatatcaaagtttatctagctatcttccgaaatagaaagcatataacttccatttatttt
tgaacaaattaaacttggtagaaataaaatctttcgatattgatttatttcgatttagtgtaac
tctattatcatctcgtgtgtcattctaggcttatagcaacagtgtaggtatgttgcaatgttgg
gttgggtcatgccgtttggatttatttccagtgattaattcagattttatttttcttcttaatta
tctacgtataacaaaatctcgttaaccgcagagtgaaattgcatgtcactcatgaatgttttga
gtataagaagtgaagtaatttgttttataaatatatgaacttatgaagatacatattgaagttgt
tttgtttgggggtaaaaaagggttatttgagtggttatatgataactttactcagaaaacgtaact
agcaaaggtaattcgaagtacctttggaatcgagtaaaatactgataactagaaaaataagata
cataatggagaaataattaaatatatttgtatttcttttttgtttaacaacgtacgttttatta
ttagctagtatacatattacaacggttacgtagatcatataatagccatttaagatgtacaacat
ctcatctgggttaacttcatttatataaaaaaaaaaacgaaatctcaacacatagtaatgtataatt
acttcagtggggtctctcttaagacttgtattgagaatatccatataaaaacaaactttgtatta
agataattaaaaattttctaatagttaggtattgggtgaagccaagattaacatggaggcagctt
taaaatgtttccttatatgatgcagccatcatttctactctactccgtagctccaaaccttct
cgtaattcacgtctctcatgctattctttttgctttcgctcctctctcatgtgaagcaataact
atctctcgatttttttttcaaataccgaaagctaaactttttcaaataaatgtcaaatatatta
atcttcgttttgtacttagtattttatttgcagctaagtatagtgagtttttaagcttactcg
tcgtatttatcatatattcatatacatatcacattagtcaaagtaataaaaaattgtttttga

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1	M	A	R	G	K	I	E	I	K	R	I	E	N	Q	T	N	R	Q
1	M	A	R	G	K	I	E	I	K	R	I	E	N	Q	T	N	R	Q
1	S	G	R	G	K	I	E	I	K	R	I	E	N	T	N	R	Q	
1	K	E	R	R	K	I	E	I	K	F	I	E	N	K	T	R	R	H
1	R	G	R	V	K	I	K	E	F	I	E	N	K	L	R	R	Y	
1	M	G	R	G	K	I	E	I	K	R	I	E	N	S	T	N	R	Q
1	M	G	R	R	R	I	E	I	Q	R	I	S	P	D	R	N	R	A
1	M	G	R	R	K	I	E	I	E	P	I	K	E	D	R	N	R	T
1	M	G	R	K	K	I	E	I	Q	R	I	T	E	R	N	R	Q	
1	M	G	R	G	K	I	E	I	K	R	I	E	N	A	N	S	R	Q
1	M	G	R	G	K	I	E	I	K	R	I	E	N	N	T	N	R	Q
1	M	G	R	G	K	I	E	I	K	R	I	E	N	K	I	N	R	Q
1	M	G	R	G	K	I	E	I	K	R	I	E	N	S	T	N	R	Q
1	M	G	V	A	K	L	E	R	Q	R	I	E	E	E	-	K	K	Q

Figure 4

Figure 1 displays the time course of the 1998/99 influenza A/H3N2 epidemic in Hong Kong. The figure consists of 12 horizontal panels, each representing a week from 1998/10/1 to 1999/01/1. Each panel shows the number of cases (bars) and the number of deaths (dots) for that week. The epidemic peaks in late 1998 and early 1999.

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Met	Ala	Thr	Ser	Leu	Phe	Phe	Met	Ser	Thr	Asp	Gln	Asn	Ser	Val	Gly	Asn	Pro	Asn	Asp	1	5	10	15	20
Leu	Leu	Lrg	Asn	Thr	Arg	Leu	Val	Val	Asn	Ser	Ser	Gly	Glu	Ile	Arg	Thr	Glu	Thr	Leu	25	30	35	40	
Lys	Ser	Arg	Gly	Arg	Lys	Pro	Gly	Ser	Lys	Thr	Gly	Gln	Gln	Lys	Gln	Lys	Lys	Pro	Thr	45	50	55	60	
Leu	Arg	Gly	Met	Gly	Val	Ala	Lys	Leu	Glu	Arg	Gln	Arg	Ile	Glu	Glu	Glu	Lys	Lys	Gln	65	70	75	80	
Leu	Ala	Ala	Ala	Thr	Val	Gly	Asp	Thr	Ser	Ser	Val	Ala	Ser	Ile	Ser	Asn	Asn	Ala	Thr	85	90	95	100	
Arg	Leu	Pro	Val	Pro	Val	Asp	Pro	Gly	Val	Val	Leu	Gln	Gly	Phe	Pro	Ser	Ser	Leu	Gly	105	110	115	120	
Ser	Asn	Arg	Ile	Tyr	Cys	Gly	Gly	Val	Gly	Ser	Gly	Gln	Val	Met	Ile	Asp	Pro	Val	Ile	125	130	135	140	
Ser	Pro	Trp	Gly	Phe	Val	Glu	Thr	Ser	Ser	Thr	Thr	His	Glu	Leu	Ser	Ser	Ile	Ser	Asn	145	150	155	160	
Pro	Gln	Met	Phe	Asn	Ala	Ser	Ser	Asn	Asn	Arg	Cys	Asp	Thr	Cys	Phe	Lys	Lys	Lys	Arg	165	170	175	180	
Leu	Asp	Gly	Asp	Gln	Asn	Asn	Val	Val	Arg	Ser	Asn	Gly	Gly	Gly	Phe	Ser	Lys	Tyr	Thr	185	190	195	200	
Met	Ile	Pro	Pro	Pro	Met	Asn	Gly	Tyr	Asp	Gln	Tyr	Leu	Leu	Gln	Ser	Asp	His	His	Gln	205	210	215	220	
Arg	Ser	Gln	Gly	Phe	Leu	Tyr	Asp	His	Arg	Ile	Ala	Arg	Ala	Ala	Ser	Val	Ser	Ala	Ser	225	230	235	240	
Ser	Thr	Thr	Ile	Asn	Pro	Tyr	Phe	Asn	Glu	Ala	Thr	Asn	His	Thr	Gly	Pro	Met	Glu	Glu	245	250	255	260	
Phe	Gly	Ser	Tyr	Met	Glu	Gly	Asn	Pro	Arg	Asn	Gly	Ser	Gly	Gly	Val	Lys	Glu	Tyr	Glu	265	270	275	280	
Phe	Phe	Pro	Gly	Lys	Tyr	Gly	Glu	Arg	Val	Ser	Val	Val	Ala	Thr	Thr	Ser	Ser	Leu	Val	285	290	295	300	
Gly	Asp	Cys	Ser	Pro	Asn	Thr	Ile	Asp	Leu	Ser	Leu	Lys	Leu							305	310			

FIG. 3

CAGACTTAAAGCTTTCGTCTTTACCTCTTECCTTCTCTCTCTATCTAAAAAGAGTTCCGAGA	64
AGAAGATCATCATCAATGGCGACTTCTCTCTTCTTCATGTCAACAGATCAAACTCCGTCGGAA	120
ACCCAAACGATCTTCTGAGAAACACCCGTCTTGTCTGTCATAGCTCCGGCGAGATCCGGACAGA	192
GACACTGAAGAGTCGTGGTCGGAAACAGGATCGAAGACAGGTCAGCAAAAAACAGAAGAAACCA	256
ACGTTGAGAGGAATGGGTGTAGCAAAGCTCGAGCGTCAGAGAATCGAAGAAGAAAGAAGCAAC	320
TCGCCGCCGCCACAGTCGGAGACACGTCATCAGTAGCATCGATCTCTAACAACGCTACCCGTTT	384
ACCCGTACCCGTAGACCCGGGTGTTGTCTACAAGGCTTCCCAAGCTCACTCGGGAGCAACAGG	448
ATCTATTGTGTGTCGAGTCGGGTCTGGGTCTAGGCTTATGATCGACCCGGTTATTTCTCCATGGGGTT	512
TTGTTGAGACCTCCTCCACTACTCATGAGCTCTCTTCAATCTCAAAATCCTCAAAATGTTTAACGC	576
TTCTTCCAATAATCGCTGTGACACTTGCTTCAAGAAGAAACGTTTGGATGGTGATCAGAATAAT	640
GTAGTTCGATCCAACGGTGGTGGATTTTCGAAATACCAATGATTCCTCCTCCGATGAACGGCT	704
ACGATCAGTATCTTCTTCAATCAGATCATCATCAGAGGAGCCAAGGTTTCCTTTATGATCATAG	768
AATCGCTAGAGCAGCTTCAGTTTCTGCTTCTAGTACTACTATTAATCCTTATTTCAACGAGGCA	832
ACAAATCATACGGGACCAATGGAGGAATTTGGGAGCTACATGGAAGGAAACCTAGAAATGGAT	896
CAGGAGGTGTGAAGGAGTACGAGTTTTTCCGGGGAAATATGGTGAAAGAGTTTCAGTGGTGGC	960
TACAACGTCGTCACCTCGTAGGTGATTGCAGTCTTAATACCATTGATTGTCTTGAAGCTTTAA	1024
ATGTTTTATCTTTCTATATTGATTTAAACAAATCGTCTCTTTAAAGAAAAAACATTTTAAGTA	1088
GATGAAAGTAAGAAACAGAAGAAAAAAGAGAGAGCCTTTTTTGGTGTATGCATCTGAGAGCT	1152
GAGTCGAAAGAAAGATTGAGCTTTTGGATTACCTTTTGGTTGTTTATTATGAGATTCTAACCT	1216
AAACACTCAGACATATATGTTCTGTTCTCTTCTTAAATTGTTGTCATGAACTTCTCAAAAAA	1280
AAAAAAAAAAAAAAAAAAAAA	1302

FIG. 2

09701023-00001

5' of the SPL gene

gtagcatcga tctctaacaa cgctacccgt ttaccctgtac cggtagaccc ggggtgttgc 59

3' of Ds element

gcta<<<cagggat gaaaacggtc ggtaacggtc ggtaaaatac-----

-----Ds element-----

tacgggattt ttcccatcct actttcatcc cgg>>>gcacaa ggcttcccaa

5' of Ds element

gctcatcggg agcaacagga tctattgtgg tggagtcggg tcgggtcagg ttatgatcga
cccgttatt tctccatggg gttttgttga gacctcctcc actactcatg agctctcttc a

FIG. 1A.

cagggat gaaaacggtc ggtaacggtc ggtaaaatac tacgggattt ttcccatcct
actttcatcc cgg

FIG. 1B.

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Figure 5 (cont)

agaataatgtagttcgatccaacgggtgggtgattttcgaaatacacaaatgattcctcctccgat
gaacggctacgatoagtatcttcttcaatcagatcatcatcagaggagccaagggttctcttat
gatcatagaatcgctagagcagcttcagtttctgottctagtaactactattaatccttatttca
acgaggcaacaaatcatacgggtactaagttatagtcattttattaatactcatatataggtatat
atgtatataactggtgatcttatttgatttaactgggtgggtttagggaccaatggaggaatttg
ggagctacatggaaggaaaccctagaaatggatcaggaggtgtgaaggagtacgagtttttcc
ggggaatatggtgaaagagtttccagtggtggctaaaaagtcgtcactcgtaggtgattgcagt
cctaataccattgattttgtcttgaagctttaaagttttctcttctatattgatttaaaaca
aatcgtctcttttaagaaaaaacatttttaagtagatgaaagtaagaaacagaagaaaaaaaaga
gagagccttttttgggtgtatgcacatctgagagctgagtcgaaagaaagattcagcttttggatta
cccttttgggtgtttattatgagattctaaccctaaacactcagacatatatgtttctgttctctt
ccttaattgttgcatgaaacttctc

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Figure 5 (cont)

agaaaaaaaaatacatataactgcgagtgctgcgactgtaactggacttgcttatttttagttga
tatgagctgagtaaaatcacgttggtcccgagaccttgctcgctacaatcggcgaatgggtctaacg
tcccgacacctgtcctcgatccgcgggtaactatattctttgcaatgtgatgcacgcgctgttac
tattggacagtggtttctcaccctacgactgagcctatgcgagtagcgacaatctccgatttgct
gtctccatggtagggattatcacaaatctctgattttttttatcaggaacaagtaaaataaatagc
tttgaggtttttgtttttttctacattcttccgccccaaaagatgtaagaaaataaaggatttgaa
accttggttctgttggttactccttttaaatcttataaaactataaatcattatatctttgatctgt
ttcacaaactaatcatattcggttgcaaagtgagaattcggtcccaactttactctttacaccgata
ctagtattatagatgtacagcatagttatccatatctagttatttagtcaaaactctatatatt
aagaggtaggttaactaattaaggagtaattgaagattatagaaagaataaaaaataaccattta
atggacagaaccaaagataactaactatcatactataatggttgaaatttcttccacgatccaatg
catggataacaacatcaatcaaatcatacattcatgctatataacatagttttcagttacaaac
tctcttttttatttatttcagttgttcttttcatgaccatattaacatcaaataatgcatttt
tttcaacgtctcttgacttacaccactaatattgacaaatlgaacatctatacgactatacac
acataagttaaaaatgcatgcaagtgttaagggaatttataacatctaagggttaataagactaa
gaaagtataaaaaataagaatacgtattatgaatttatgatatactttactaatctttttgaaaaa
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atatagtacctggaaataacagaaaaataaaaacacaggtaagtactttgcctgagctagtatat
gaacactaaagagatacacacacacaaaaagagagcagaaacaaaacacacacacttaaaagctt
tcgtctttacctc

#1

ttcccttctctctctctctatatotaaaaagagttccgagaagaagatcatcatcaatggogacttct
ctcttctctctctctctctcaacagatcaaaactccgtcggaancccaaacgatcttctgagaaacacc
gtcttgctcgtaacagctccggcgagatccggacagagacactgaagagtcgtggtcggaancc
aggatcgaagacaggtcagcaaaaacagaaagaaacacgttgagaggaatgggtgtagcaaaag
ctcgagcgtcagagaatcgaagaagaaaagaagcaactcgccgcgcacagtcggagacacgt
catcagtagcatcgatctctaaacacgctacccgttttaaccgtacccggtagacccgggtgttgt
gctacaaggcttcccaagctcactcgggagcaacaggatctattgtggtggagtcgggtcgggt
caggttatgatcgaccgggttatttctccatgggggttttgttgagacctcctccactactcatg
agctctcttcaatctcaaatcctcaaatgtttaogetttcttcaataatcgctgtgacacttg
cttcaagggttggttggttttttaatcggttttcatcaacatgattgatataatagtttttgc
acttgaaaaagtttgatttttatttatgtaaaaaactgcagaagaaacggtttggatggtgac

FIGURE 5

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cggatcccaagaatctttctatgcctgcctaaacccagcaatataaatcaaaccttcacacgct
tcggttcttcttttacacgtgccggaacccctagtagtagccgcccaatgaccatctaaa
gtggtccccgtgatgacacgtgtcagttggaccactatccgtaacttaacatgaaagcacatgt
ggggtccctctttcgctctttgccctaccagttccttgctctagcccacatacaatctacgcg
gtatctatatcaaagtttatctagctattttccgaaatagaagcatatacttccatttatttt
tgaacaaattaaacttggtagaaataaaatctttcgatattgatttatttccgatttagtgtaat
tctattatcatctcgctgtctcattcttaggcttatagcaacagtgtaggtatggttgcaatggttg
gttgggtcatgccgtttggatttatttccagtgattaattcagattttatttttcttcttaatta
tctacgtataacaaaatctcgctaaccgcagagtgaatttgcattgtcactcatgaatgttttga
gtataagaagtgaagtaatttgttttataaatatatgaacttatgaagatacatattgaagttgt
tttgtttgggggtaaaaaagggttatctgagtggtatatgataactttactcagaaaacgtaact
agcaaaggtaattcgaagtacctttggaatcgagtaataactgataactagaaaaataagata
cataatggagaaaataattaaatatatttgtatttcttttttgtttaacaacgtacgttttatta
ttagctagtatacatttacaacgggtacgtagatcatataatagccatttaagatgtacaacat
ctcatctgggttacttcatttatataaaaaaaaaaacgaaatctcaacacatagtaattgtataatt
acttcagtggggcttctcttaagacttgtatttgagaatatccatataaaaacaaactttgtatta
agataattaaaaattttctaattagtaggtattgggctgaagccaagattaacatggaggcagctt
taaaatgtttcttatatgatgcagccatcatttctactctactccgtagctccaaaccccttct
cgtaattcaagtcctctcatgtctattctttttgctttcgtctcctctcatgtgaagcaataact
atctctcgatttttttttcaaataccgaaagctaactttttcaaataaatgtcaaataatatta
attttcgttttgtatttagtattttatttgcagctaagtatagttagtattttaagcttactcg
tcgtatttatcatatattcatatacatatcacattagtcaaagtaataaaaaatttgtttttga

SEQUENCE "E207D" 500

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AP3
DEFA
AG_
MCM1
SRF
GLO
RLM1-yeast
SMP1-yeast
MEF2D
AGL5
FBP11
BOAP1
AGL11
SPL

1	M	A	R	G	K	I	E	I	K	R	I	E	N	Q	T	N	R	Q
1	M	A	R	G	K	I	E	I	K	R	I	E	N	Q	T	N	R	Q
1	S	G	R	G	K	I	E	I	K	R	I	E	N	T	N	R	Q	
1	K	E	R	R	K	I	E	I	K	F	I	E	N	K	T	R	R	H
1	R	G	R	V	K	I	E	I	K	F	I	E	N	K	L	R	R	Y
1	M	G	R	G	K	I	E	I	K	R	I	E	N	S	T	N	R	Q
1	M	G	R	R	K	I	E	I	Q	R	I	S	D	R	N	R	A	
1	M	G	R	R	K	I	E	I	E	P	I	K	D	R	N	R	T	
1	M	G	R	K	K	I	E	I	Q	R	I	T	E	R	N	R	Q	
1	M	G	R	G	K	I	E	I	K	R	I	E	N	A	N	S	R	Q
1	M	G	R	G	K	I	E	I	K	R	I	E	N	N	T	N	R	Q
1	M	G	R	G	K	I	E	I	K	R	I	E	N	K	I	N	R	Q
1	M	G	R	G	K	I	E	I	K	R	I	E	N	S	T	N	R	Q
1	M	G	V	A	K	L	E	R	Q	R	I	E	E	E	K	K	Q	

Figure 4

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Met Ala Thr Ser Leu Phe Phe Met Ser Thr Asp Gln Asn Ser Val Gly Asn Pro Asn Asp
1 5 10 15 20
Leu Leu Lrg Asn Thr Arg Leu Val Val Asn Ser Ser Gly Glu Ile Arg Thr Glu Thr Leu
25 30 35 40
Lys Ser Arg Gly Arg Lys Pro Gly Ser Lys Thr Gly Gln Gln Lys Gln Lys Lys Pro Thr
45 50 55 60
Leu Arg Gly Met Gly Val Ala Lys Leu Glu Arg Gln Arg Ile Glu Glu Glu Lys Lys Gln
65 70 75 80
Leu Ala Ala Ala Thr Val Gly Asp Thr Ser Ser Val Ala Ser Ile Ser Asn Asn Ala Thr
85 90 95 100
Arg Leu Pro Val Pro Val Asp Pro Gly Val Val Leu Gln Gly Phe Pro Ser Ser Leu Gly
105 110 115 120
Ser Asn Arg Ile Tyr Cys Gly Gly Val Gly Ser Gly Gln Val Met Ile Asp Pro Val Ile
125 130 135 140
Ser Pro Trp Gly Phe Val Glu Thr Ser Ser Thr Thr His Glu Leu Ser Ser Ile Ser Asn
145 150 155 160
Pro Gln Met Phe Asn Ala Ser Ser Asn Asn Arg Cys Asp Thr Cys Phe Lys Lys Lys Arg
165 170 175 180
Leu Asp Gly Asp Gln Asn Asn Val Val Arg Ser Asn Gly Gly Gly Phe Ser Lys Tyr Thr
185 190 195 200
Met Ile Pro Pro Pro Met Asn Gly Tyr Asp Gln Tyr Leu Leu Gln Ser Asp His His Gln
205 210 215 220
Arg Ser Gln Gly Phe Leu Tyr Asp His Arg Ile Ala Arg Ala Ala Ser Val Ser Ala Ser
225 230 235 240
Ser Thr Thr Ile Asn Pro Tyr Phe Asn Glu Ala Thr Asn His Thr Gly Pro Met Glu Glu
245 250 255 260
Phe Gly Ser Tyr Met Glu Gly Asn Pro Arg Asn Gly Ser Gly Gly Val Lys Glu Tyr Glu
265 270 275 280
Phe Phe Pro Gly Lys Tyr Gly Glu Arg Val Ser Val Val Ala Thr Thr Ser Ser Leu Val
285 290 295 300
Gly Asp Cys Ser Pro Asn Thr Ile Asp Leu Ser Leu Lys Leu
305 310

FIG. 3

CAGACTTAAAGCTTTCGTCTTTACCTCTTECCTTCTCTCTCTATCTA	64
AGAAGATCATCATCAATGGCGACTTCTCTCTTCTTCAATGTCAACAGATCA	120
ACCCAAACGATCTTCTGAGAAACACCCGCTTGTGTCGTCATAGCTCCGGCC	192
GACACTGAAGAGTCGTGGTCGGAAACAGGATCGAAGACAGGTCAAGAAAC	256
ACGTTGAGAGGAATGGGTGTAGCAAAGCTCGAGCGTCAGAGAATCGAAGA	320
TCGCCGCCGCCACAGTCGGAGACACGTCATCAGTAGCATCGATCTCTAAC	384
ACCCGTACCCGTAGACCCGGGTGTTGTGCTACAAGGCTTCCCAAGCTCA	448
ATCTATTGTGGTGGAGTCGGGTTCGGGTTCAGGTTATGATCGACCCGGT	512
TTGTTGAGACCTCCTCCACTACTCATGAGCTCTCTCAATCTCAAATCCT	576
TTCTTCCAATAATCGCTGTGACACTTGCTTCAAGAAGAAACGTTTGGAT	640
GTAGTTCGATCCAACGGTGGTGGATTTTCGAAATACACAATGATTCCCT	704
ACGATCAGTATCTTCTTCAATCAGATCATCATCAGAGGAGCCAAGGTT	768
AATCGCTAGAGCAGCTTCAGTTTCTGCTTCTAGTACTACTATTAATCCT	832
ACAAATCATACGGGACCAATGGAGGAATTTGGGAGCTACATGGAAGGAA	896
CAGGAGGTGTGAAGGAGTACGAGTTTTTCCGGGGAATATGGTGAAAGAG	960
TACAACGTCGTCCTCGTAGGTGATTGCAGTCTTCAATACCATTGATTGT	1024
ATGTTTTATCTTTCTATATTGATTTAAACAAATCGTCTCTTTAAAGAAA	1088
GATGAAAGTAAGAAACAGAAGAAAAAAGAGAGAGCCTTTTTGGTGATGC	1152
GAGTCGAAAGAAAGATTTCAGCTTTTGGATTACCTTTTGGTTGTTTATT	1216
AAACACTCAGACATATATGTTCTGTTCTCTTACCTTAATTGTTGTCATG	1280
AAAAAAAAAAAAAAAAAAAAA	1302

FIG. 2

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5' of the *SPL* gene

gtagcatcga tctctaacaa cgctaccegt ttaccctgac cggtagaccc ggggtgttgc 59

3' of Ds element

gcta<<<cagggat gaaaacggtc ggtaacggtc ggtaaaatac-----

-----Ds element-----

tacgggattt ttcccatcct actttcatcc cgg>>>gctacaa ggcttcccaa

5' of Ds element

gctcatcggg agcaacagga tctattgtg tggagtcggg tcgggtcagg ttatgatcga
cccggttatt tctccatggg gttttgttga gacctcctcc actactcatg agctctcttc A

FIG. 1A.

cagggat gaaaacggtc ggtaacggtc ggtaaaatac tacgggattt ttcccatcct
actttcatcc cgg

FIG. 1B.

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